

IN THE CLAIMS:

Please amend the claims as follows:

Please cancel Claims 98-112, 114-117, and 121, *i.e.*, all of the pending claims, without prejudice and add new Claims 122-155 as follows:

1.-121. (Cancelled)

122. (New) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71, 64, 93, 23, 58, and 36, wherein the presence of said protease-encoding nucleic acid in said biological sample in comparison indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease.
123. (New) The method of Claim 122, wherein said mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V) or said mutation at codon 90 is a substitution of methionine (M) for leucine (L).
124. (New) The method of Claim 123, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 73, 55, 48, 20, 43, 53, 90, 13, 23, 84, 53, 74, 60, 33, 36, 35, 32, and 46, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, 54, 82, 85, 84, 20, 72, 62, 74, 53, 48, 23, 58, 36, 64, 77, and 93.
125. (New) The method of claim 124, wherein said difference in said HIV's susceptibility to amprenavir relative to a reference HIV is greater than 10 fold.
126. (New) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said patient a nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 33,

23, 84, 32, 53, 90, 37, 71, 10, 54, 61, 11, and 46, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 89, 53, 84, 33, 92, 95, 54, 58, 46, 82, 36, 10, 62, 74, 15, 47, 66, 32, 55, 53, 13, and 69, wherein the presence of said protease-encoding nucleic acid in said biological sample in comparison indicates a difference in said HIV protease's susceptibility to amprenavir relative to a reference HIV protease.

127. (New) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 73, 55, 53, 23, 33, and 39, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 55, 85, 66, 33, 73, 23, and 58, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease.
128. (New) The method of Claim 127, wherein said mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V) or said mutation at codon 90 is a substitution of methionine (M) for leucine (L).
129. (New) The method of Claim 127, wherein said protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.
130. (New) The method of Claim 129, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 23, 73, 53, 33, and 39, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 66, 33, and 73, and wherein said protease inhibitor is saquinavir.
131. (New) The method of Claim 130, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 23, 73, 53, and 33, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 66, 33, and 73, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to saquinavir.

132. (New) The method of Claim 129, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, and 46, and wherein said protease inhibitor is indinavir.
133. (New) The method of Claim 132, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, and 46, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to indinavir.
134. (New) The method of Claim 129, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 73, 55, 53, 23, and 33, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, 85, 53, 23, 58, and 77.
135. (New) The method of claim 127, wherein said difference in said HIV protease's susceptibility to said protease inhibitor relative to a reference HIV is greater than 10 fold.
136. (New) The method of claim 128, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 23, 53, 33, and 35, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 23, and 58, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to saquinavir.
137. (New) The method of claim 128, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 73, 55, and 53, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, and 85, and wherein said difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease is a decrease in susceptibility to indinavir.
138. (New) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said patient a nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 33,

23, 53, and 11, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 89, 53, 33, 92, 95, 58, 66, and 55, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates a difference in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease.

139. (New) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said HIV-infected patient a nucleic acid encoding an HIV protease that comprises a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 73, 55, 48, 20, 43, 53, 90, 13, 84, 23, 33, 74, 32, 39, 60, 36, and 35, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 54, 84, 82, 46, 13, 74, 55, 85, 20, 72, 62, 66, 84, 48, 33, 73, 71, 64, 93, 23, 58, and 36, wherein the presence of said protease-encoding nucleic acid in said biological sample indicates an increase in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease.
140. (New) The method of Claim 139, wherein said mutation at codon 82 is a substitution of alanine (A), phenylalanine (F), serine (S), or threonine (T) for valine (V) or said mutation at codon 90 is a substitution of methionine (M) for leucine (L).
141. (New) The method of Claim 139, wherein said protease inhibitor is selected from the group consisting of indinavir, amprenavir, and saquinavir.
142. (New) The method of Claim 141, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 84, 48, 23, 73, 53, 33, 74, 20, 90, 32 and 39, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 66, 84, 54, 48, 33, 73, 20, 71, 64 and 93, and wherein said protease inhibitor is saquinavir.
143. (New) The method of Claim 142, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at codon 32 or codon 39, or a mutation at codon 90 and a secondary mutation at codon 64 or codon 93.

144. (New) The method of Claim 141, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 54, 84, 82, 46, 13, 74, and wherein said protease inhibitor is indinavir.
145. (New) The method of Claim 141, wherein said nucleic acid has a mutation at codon 90 and a secondary mutation at codon 13 or codon 74.
146. (New) The method of Claim 139, wherein said nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 73, 55, 48, 20, 43, 53, 90, 13, 23, 84, 53, 74, 60, 33, 36, 35, 32, and 46, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 95, 55, 54, 82, 85, 84, 20, 72, 62, 74, 53, 48, 23, 58, 36, 64, 77, and 93.
147. (New) The method of claim 146, wherein said increase in said HIV protease's susceptibility to said protease inhibitor relative to a reference HIV protease is greater than 10 fold.
148. (New) The method of claim 147, wherein the nucleic acid has a mutation at codon 82 and a secondary mutation at codon 32 or codon 46, or a mutation at codon 90 and a secondary mutation at codon 64, codon 77, or codon 93, and wherein said protease inhibitor is saquinavir.
149. (New) A method of assessing the effectiveness of protease antiretroviral therapy of a patient infected with HIV, said method comprising detecting in a biological sample from said patient a nucleic acid encoding HIV protease having a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 33, 23, 84, 32, 53, 90, 37, 71, 10, 54, 61, 11, and 46, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 89, 53, 84, 33, 92, 95, 54, 58, 46, 82, 36, 10, 62, 74, 15, 47, 66, 32, 55, 53, 13, and 69, wherein the presence of said protease-encoding nucleic acid in said biological sample in comparison to a reference sample indicates an increase in said HIV protease's susceptibility to a protease inhibitor relative to a reference HIV protease.
150. (New) A test vector, comprising:
- (a) a segment derived from HIV from an HIV-infected patient, which segment comprises a protease-encoding nucleic acid, wherein said protease-encoding

nucleic acid has a mutation at codon 82 and a secondary mutation at a codon selected from the group consisting of codons 73, 55, 53, 23, 33, and 39, or a mutation at codon 90 and a secondary mutation at a codon selected from the group consisting of codons 53, 95, 55, 85, 66, 33, 73, 23, and 58; and

- (b) an indicator gene, wherein the amount of expression of said indicator gene in a host cell depends upon the activity of said HIV protease.